In the Specification:

Please amend the specification as shown:

Please delete the paragraph on page 44, line 1 to 12, and replace it with the following paragraph:

Quantitative RT-PCR - Microarray data were confirmed using real time PCR analysis. First strand cDNA synthesis was performed on 0.5µg total RNA using random hexamer primers and SuperscriptII RT (Invitrogen Life Technologies). Quantitative PCR was performed on a ABIPrism 7700 cycler (Applied Biosystems) using a Taqman PCR kit. Serial dilutions of cDNA were used to generate standard curves of threshold cycles versus the logarithms of concentration for ß-actin, CRH receptor 1 (Crh-R1), CRH receptor 2 (Crh-R2), neurotensin receptor 1 (Ntsr1), neurotensin receptor 2 (Ntsr2), neurotensin receptor 3 (Ntsr3), 11ß-hydroxysteroid dehydrogenase 1 (Hsd11B1), serum/glucocorticoid regulated kinase (Sgk) and the genes of interest (see table for sequences of primers **(SEQ ID NOS 42-65, respectively in order of appearance)**). A linear regression line calculated from the standard curves allowed the determination of transcript levels in RNA samples from the different treatment groups at each brain area.